

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

~~08/993002~~ 08/487,032

Art Unit / Team No. :

01PE

Date Processed by STIC:

1/30/98

RECEIVED

MAR 09 1998

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SERVICE CENTER

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2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/993,002

DATE: 01/31/98
TIME: 13:03:17

INPUT SET: S23123.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: DOUGLAS SMITH et al

(ii) TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

Does Not Comply
Corrected Diskette Needed

RELATING TO HELICOBACTER PYLO
DIAGNOSTICS AND THERAPEUTICS

(iii) NUMBER OF SEQUENCES: 10031

mainly - DON'T use TAB's

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: CD-ROM ISO9660

(B) COMPUTER: mandatory response

(C) OPERATING SYSTEM: mandatory response

(D) SOFTWARE: mandatory response

They cause
misalignment
(all text must be
visible on page)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER

(B) FILING DATE:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

duplicate (headers and
responses)

(ix) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(x) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD

(B) STREET: 28 State Street

(C) CITY: Boston

(D) STATE: Massachusetts

(E) COUNTRY: USA

(F) ZIP: 02109-1875

This section
belongs above

(iv) COMPUTER READABLE FORM;
section

(xi) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mandragouras, Amy E.

(B) REGISTRATION NUMBER: 36,207

(C) REFERENCE/DOCKET NUMBER: GTN-018

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/993,002DATE: 01/31/98
TIME: 13:03:37

INPUT SET: S23123.raw

47
48 (ix) TELECOMMUNICATION INFORMATION:
49 (A) TELEPHONE: (617)227-7400
50 (B) TELEFAX: (617)742-4214
51
52 (2) INFORMATION FOR SEQ ID NO:1:
53
54 (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 789 base pairs
56 (B) TYPE: nucleic acid
57 (C) STRANDEDNESS: double
58 (D) TOPOLOGY: circular
59
60 (ii) MOLECULE TYPE: DNA (genomic)
61
62 (iii) HYPOTHETICAL: NO
63
64 (iv) ANTI-SENSE: NO
65
66 (vi) ORIGINAL SOURCE:
67 (A) ORGANISM: Helicobacter pylori
68
69 (ix) FEATURE:
70 (A) NAME/KEY: misc_feature
71 (B) LOCATION: 1...789
72
73 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
74
75 ATGCTCCGCT CTCTCTATAG TGCCACTTCA GGGATGCTCG CCCAACAAAC GCACATTGAC 60
76 ACCACTTCAA ACAACATCGC CAATGTCAAT ACCACCGGGT TTAATAAATC TCGCGCGGAT 120
77 TTTAACGACT TGTTTTACCA AGCGATGCAA TACGCCGGCA CCAACACAAG CAACACGACT 180
78 TTATCGCCAG ATGGCATGGA AGTGGGCTTA GGCGTACGCC CTAGTGCGAT TACCAAAATG 240
79 TTTTCGCAAG GCAGCCCTAA AGAAACGGAG AATAATTTAG ATATTGCTAT TACAGGTAAA 300
80 GGCTTTTTTC AAGTCCAGCT TCCTGTATGGC ACTACCGCTT ACACAAGGAG CGGGAATTTT 360
81 AAGCTAGACG AGCAGGGCAA TCTTGTAACA AGCGAGGGCT ATCTCCTCAT CCCTCAAATC 420
82 ACTTTACCCG AAGACACCAC GCAAGTGAAT ATCGGTGTGG ATGGCACGGT GAGCGTGACT 480
83 CAAGGCTTGC AAACGACTTC TAACGTGATC GGGCAAATCA CTTTGGCTAA TTTTGTCAAT 540
84 CCGGCGGGGC TTCATTCTAT GGGGGATAAT TTGTTTTCCA TCACCAACGC TAGCGGCGAT 600
85 GCGATTGTGG GCAACCCGGA TTCTCAAGGC TTAGGCAAGT TAAGGCAAGG CTTTTTGGAG 660
86 CTTAGTAACG TGAGATTGGT AGAAGAAATG ACAGATCTAA TCACCGCTCA AAGGGCTTAT 720
87 GAAGCCAATT CTAAAAGCAT TCAAACCGCT GATGCCATGC TCCAAACAGT CAATTCCTTC 780
88 AAACGCTAA 89
90 (2) INFORMATION FOR SEQ ID NO:2:
91
92 (i) SEQUENCE CHARACTERISTICS:
93 (A) LENGTH: 816 base pairs
94 (B) TYPE: nucleic acid
95 (C) STRANDEDNESS: double
96 (D) TOPOLOGY: circular
97
98 (ii) MOLECULE TYPE: DNA (genomic)
99

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/993,002DATE: 01/31/98
TIME: 13:03:40

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100 (iii) HYPOTHETICAL: NO
101
102 (iv) ANTI-SENSE: NO
103
104 (vi) ORIGINAL SOURCE:
105 (A) ORGANISM: Helicobacter pylori
106
107 (ix) FEATURE:
108 (A) NAME/KEY: misc_feature
109 (B) LOCATION: 1...816
110
111 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
112
113 TTGTTAAGTT TAGTTAAAGG GAAAACCATG CTCCGCTCTC TCTATAGTGC CACTTCAGGG 60
114 ATGCTCGCCC AACAAACGCA CATTGACACC ACTTCAAACA ACATCGCCAA TGTCAATACC 120
115 ACCGGGTTTA AAAAATCTCG CGCGGATTTT AACGACTTGT TTTACCAAGC GATGCAATAC 180
116 GCCGGCACCA ACACAAGCAA CACGACTTTA TCGCCAGATG GCATGGAAGT GGGCCTTGGC 240
117 GTACGCCCTA GTGCGATTAC CAAAATGTTT TCGCAAGGCA GCCCTAAAGA AACGGAGAAT 300
118 AATTTAGATA TTGCTATTAC AGGTAAAGGC TTTTTTCAAG TCCAGCTTCC TGATGGCACT 360
119 ACCGCTTACA CAAGGAGCGG GAATTTCAAG CTAGACGAGC AGGGCAATCT TGTAACAAGC 420
120 GAGGGCTATC TCCTCATCCC TCAAATCACT TTACCCGAAG ACACCACGCA AGTGAATATC 480
121 GGTGTGGATG GCACGGTGAG CGTGA CTCAA GGCTTGCAAA CGACTTCTAA CGTGATCGGG 540
122 CAAATCACTT TGGCTAATTT TGTCAATCCG GCGGGGCTTC ATTCTATGGG GGATAATTTG 600
123 TTTTCCATCA CCAACGCTAG CGGCGATGCG ATTGTGGGCA ACCCGGATTC TCAAGGCTTA 660
124 GGCAAGTTAA GGCAAGGCTT TTTGGAGCTT AGTAACGTGA GATTGGTAGA AGAAATGACA 720
125 GATCTAATCA CCGCTCAAAG GGCTTATGAA GCCAATTCTA AAAGCATTCA AACCCTGTAT 780
126 GCCATGCTCC AAACAGTCAA TTCCCTCAAA CGCTAA 816
127
128 (2) INFORMATION FOR SEQ ID NO:3:
129
130 (i) SEQUENCE CHARACTERISTICS:
131 (A) LENGTH: 837 base pairs
132 (B) TYPE: nucleic acid
133 (C) STRANDEDNESS: double
134 (D) TOPOLOGY: circular
135
136 (ii) MOLECULE TYPE: DNA (genomic)
137
138 (iii) HYPOTHETICAL: NO
139
140 (iv) ANTI-SENSE: NO
141
142 (vi) ORIGINAL SOURCE:
143 (A) ORGANISM: Helicobacter pylori
144
145 (ix) FEATURE:
146 (A) NAME/KEY: misc_feature
147 (B) LOCATION: 1...837
148
149 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
150
151 TCTTATTTTT GTTATAATCT TAGGTTGTTA AGTTTAGTTA AAGGGAAAAC CATGCTCCGC 60
152 TCTCTCTATA GTGCCACTTC AGGGATGCTC GCCCAACAAA CGCACATTGA CACCACTTCA 120

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/993,002DATE: 01/31/98
TIME: 13:03:43

INPUT SET: S23123.raw

153	AACAACATCG	CCAATGTCAA	TACCACCGGG	TTTAAAAAAT	CTCGCGCGGA	TTTTAACGAC	180
154	TTGTTTTACC	AAGCGATGCA	ATACGCCGGC	ACCAACACAA	GCAACACGAC	TTTATCGCCA	240
155	GATGGCATGG	AAGTGGGCCT	TGGCGTACGC	CCTAGTGCGA	TTACCAAAAT	GTTTTTCGAA	300
156	GGCAGCCCTA	AAGAAACGGA	GAATAATTTA	GATATTGCTA	TTACAGGTAA	AGGCTTTTTT	360
157	CAAGTCCAGC	TTCTTGATGG	CACTACCGCT	TACACAAGGA	GCGGGAATTT	CAAGCTAGAC	420
158	GAGCAGGGCA	ATCTTGTAAC	AAGCGAGGGC	TATCTCCTCA	TCCCTCAAAT	CACTTTACCC	480
159	GAAGACACCA	CGCAAGTGAA	TATCGGTGTG	GATGGCACGG	TGAGCGTGAC	TCAAGGCTTG	540
160	CAAACGACTT	CTAACGTGAT	CGGGCAAATC	ACTTTGGCTA	ATTTTGTCAA	TCCGGCGGGG	600
161	CTTCATTCTA	TGGGGGATAA	TTTGTTTTCC	ATCACCACG	CTAGCGGCGA	TGCGATTGTG	660
162	GGCAACCCCG	ATTCTCAAGG	CTTAGGCAAG	TTAAGGCAAG	GCTTTTTTGA	GCTTAGTAAC	720
163	GTGAGATTGG	TAGAAGAAAT	GACAGATCTA	ATCACCGCTC	AAAGGGCTTA	TGAAGCCAAT	780
164	TCTAAAAGCA	TTCAAACCGC	TGATGCCATG	CTCCAAACAG	TCAATTCCCT	CAAACGC	837

165

166 (2) INFORMATION FOR SEQ ID NO:4:

167

168 (i) SEQUENCE CHARACTERISTICS:

169 (A) LENGTH: 315 base pairs

170 (B) TYPE: nucleic acid

171 (C) STRANDEDNESS: double

172 (D) TOPOLOGY: circular

173

174 (ii) MOLECULE TYPE: DNA (genomic)

175

176 (iii) HYPOTHETICAL: NO

177

178 (iv) ANTI-SENSE: NO

179

180 (vi) ORIGINAL SOURCE:

181 (A) ORGANISM: Helicobacter pylori

182

183 (ix) FEATURE:

184 (A) NAME/KEY: misc_feature

185 (B) LOCATION: 1...315

186

187 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

188

189	TTAAGGGAAA	GCATGTTTTT	ATCTTCTTTT	GATATTAGCG	GTTATGGTTT	GTCCGCCCAA	60
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190	CGCTTAAGGG	CTAATTTGAT	TTCTTCTAAT	ATCGCTAACG	CTAACACCAC	GCGCACGAGC	120
-----	------------	------------	------------	------------	------------	------------	-----

191	GAAGGAGGTC	CTTATAGGAG	ACAAGAAGCG	GTGTTTAGGG	CTTTTGATTT	CAATGAGATT	180
-----	------------	------------	------------	------------	------------	------------	-----

192	TTAAACCAAA	AAATCGCCCA	AAACAATCAA	ATCATCCCTT	ATGAAGACCC	TTTAGATGAA	240
-----	------------	------------	------------	------------	------------	------------	-----

193	GGCGATGACA	ACCCCTTAAT	CCCCATTACA	AGCGTGCTGG	TGGATAAGAT	TGCGCGCGAT	300
-----	------------	------------	------------	------------	------------	------------	-----

194	GATAGTGATC	CGTTG					315
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195

196 (2) INFORMATION FOR SEQ ID NO:5:

197

198 (i) SEQUENCE CHARACTERISTICS:

199 (A) LENGTH: 486 base pairs

200 (B) TYPE: nucleic acid

201 (C) STRANDEDNESS: double

202 (D) TOPOLOGY: circular

203

204 (ii) MOLECULE TYPE: DNA (genomic)

205

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/993,002DATE: 01/31/98
TIME: 13:03:47

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206 (iii) HYPOTHETICAL: NO
207
208 (iv) ANTI-SENSE: NO
209
210 (vi) ORIGINAL SOURCE:
211 (A) ORGANISM: Helicobacter pylori
212
213 (ix) FEATURE:
214 (A) NAME/KEY: misc_feature
215 (B) LOCATION: 1...486
216
217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
218
219 ATGTTTTTTAT CTTCTTTTGA TATTAGCGGT TATGGTTTGT CCGCCCAACG CTTAAGGGCT 60
220 AATTTGATTT CTTCTAATAT CGCTAACGCT AACACCACGC GCACGAGCGA AGGAGGTCCT 120
221 TATAGGAGAC AAGAAGCGGT GTTTAGGGCT TTTGATTTCA ATGAGATTTT AAACCAAAAA 180
222 ATCGCCCAAA ACAATCAAAT CATCCCTTAT GAAGACCCTT TAGATGAAGG CGATGACAAC 240
223 CCCTTAATCC CCATTACAAG CGTGGTGGTG GATAAGATTG CGCGCGATGA TAGTGAGCCG 300
224 TTGATGAAAT ACGATCCCAG CCACCCTGAC GCTAACGCTC AAGGCTATGT GGCTTACCCC 360
225 AATGTGAATG CCGTGGTTGA AATGGCGGAC TTAGTGGAAG CGACTAGAGC TTATCAGGCT 420
226 AATGTTGCAG CCTTTCAAAG CGCTAAAAAC ATGGCGCAA ATGCGATTGG CATGTTACAA 480
227 ACATGA 486
228
229 (2) INFORMATION FOR SEQ ID NO:6:
230
231 (i) SEQUENCE CHARACTERISTICS:
232 (A) LENGTH: 330 base pairs
233 (B) TYPE: nucleic acid
234 (C) STRANDEDNESS: double
235 (D) TOPOLOGY: circular
236
237 (ii) MOLECULE TYPE: DNA (genomic)
238
239 (iii) HYPOTHETICAL: NO
240
241 (iv) ANTI-SENSE: NO
242
243 (vi) ORIGINAL SOURCE:
244 (A) ORGANISM: Helicobacter pylori
245
246 (ix) FEATURE:
247 (A) NAME/KEY: misc_feature
248 (B) LOCATION: 1...330
249
250 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
251
252 ATGCAAGCCA TACACAATGA TAAAAGCTTA TTGAGTCCTT TCTCTGAGCT TAACACGGAC 60
253 AACAGGACTA AAAGAGGAGA ATCGGGTAGC ACCTTTAAAG AACAAAAAGG TGGGGAGTTT 120
254 TCTAAACTCT TGAAACAATC TATCAACGAG CTTAACAACA CTCAAGAGCA GTCTGATAAA 180
255 GCCTTAGCCG ACATGGCGAC AGGGCAGATC AAGGACTTGC ACCAAGCGGC TATCGCCATA 240
256 GGGAAAGGCTG AAACGAGCAT GAAACTCATG CTTGAAGTGC GTAACAAAGC GATCAGTGCT 300
257 TATAAAGAGC TTTTAAGAAC GCAGATCTAA 330
258

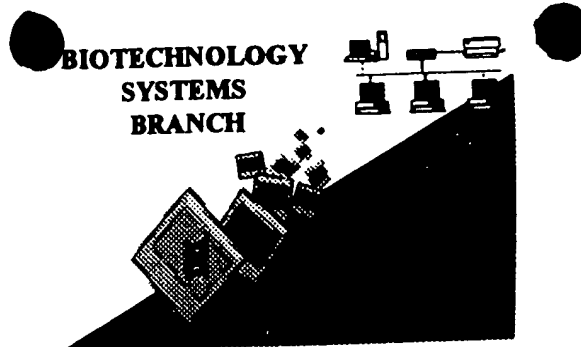
PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/993,002

DATE: 01/31/98
TIME: 13:03:50

INPUT SET: S23123.raw

Line	Error	Original Text
15	Mandatory Value Not Present	(B) COMPUTER:
16	Mandatory Value Not Present	(C) OPERATING SYSTEM:
17	Mandatory Value Not Present	(D) SOFTWARE:



Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CFR 1.821 through 1.825). Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested from the following locations:

- 1) Dial-up access through the Internet. Location is <ftp://ftp.uspto.gov>
The software is in current directory: [pub/checker/](ftp://ftp.uspto.gov/pub/checker/)
Download all the files. Cost: Free-of-charge
- 3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
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VISA/ Mastercard/ Charge- Charges can be faxed to 703-306-2737
PTO Deposit Account

For Further Information, Contact: Arti Shah at 703-308-4212